

BLAST Basic Local Alignment Search Tool

Job Title: lcl|30069 (1209 letters)

•

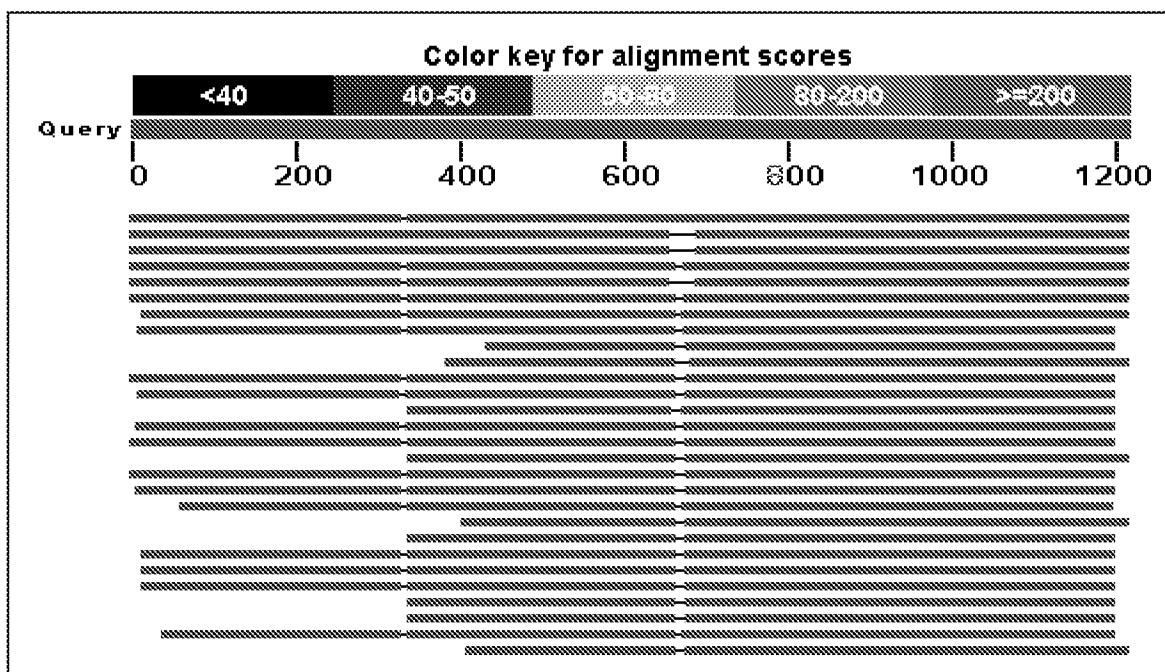
[Please try our new design!](#)

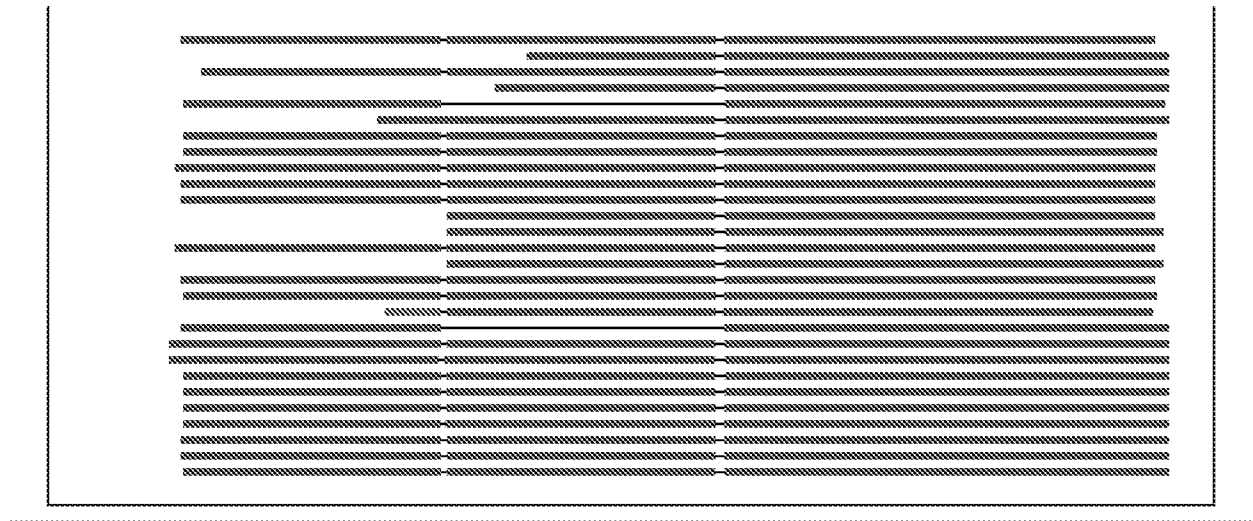
BLASTN 2.2.18+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14. RID: D4WE0DPM01N Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 7,426,127 sequences; 24,899,347,697 total letters

Query= Length=1209

Distribution of 260 Blast Hits on the Query Sequence





[Distance tree of results](#) [NEW](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure 

Sequences producing significant alignments:

(Click headers to sort columns)

EU580100.1	Mutant HIV-2 isolate VCP DeltaV3(6,6)+a-p16 1559 2138 99% 0.0 98%
	from USA modified envelope glycoprotein
	(env) gene, complete cds
EU580103.1	Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a- 1122 2020 97% 0.0 97%
	p16B from USA modified envelope
	glycoprotein (env) gene, complete cds
EU580102.1	Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a- 1122 2020 97% 0.0 97%
	p16A from USA modified envelope
	glycoprotein gene, complete cds
EU580099.1	HIV-2 isolate vcp from USA envelope 981 2151 98% 0.0 99%
	glycoprotein (env) gene, complete cds
EU580101.1	Mutant HIV-2 isolate VCP DeltaV3(1,1)+a-p36 920 2036 96% 0.0 98%
	from USA modified envelope glycoprotein
	(env) gene, complete cds
J03654.1	Human immunodeficiency virus type 2, 893 1995 98% 0.0 97%
	isolate HIV2FG
U05355.1	Human immunodeficiency virus type 2 isolate 632 1476 97% 1e- 91%
	HIV2CAM3, Guinea Bissau gp160 envelope
	(env) gene, complete cds 177
U05351.1	Human immunodeficiency virus type 2 isolate 617 1434 96% 3e- 89%
	HIV2CBL22 gp160 envelope (env) gene,
	complete cds 173
AF170050.1	HIV-2 isolate 96325 from France envelope 614 884 62% 4e- 88%
	glycoprotein (env) gene, partial cds 172
AF170042.1	HIV-2 isolate 96308 from France envelope 612 992 66% 1e- 91%
	glycoprotein (env) gene, partial cds 171
U05352.1	Human immunodeficiency virus type 2 isolate 599 1497 97% 1e- 93%
	HIV2CBL23 gp160 envelope (env) gene,
	complete cds 167
DQ213030.1	HIV-2 isolate P2-1996 from Sweden envelope 597 1347 96% 4e- 87%
	glycoprotein (env) gene, partial cds 167
AF170047.1	HIV-2 isolate 96330 from France envelope 597 973 69% 4e- 87%
	glycoprotein (env) gene, partial cds 167
U05350.1	Human immunodeficiency virus type 2 isolate 595 1380 96% 1e- 89%
	HIV2CBL21 gp160 envelope (env) gene,
	complete cds 166
AY509259.1	HIV-2 isolate MCN13, complete genome 593 1486 97% 5e- 93%
	166
AJ001162.1	Human Immunodeficiency Virus Type 2 partial 590 1041 71% 6e- 91%
	envelope sequence, isolate sar from child
	in vertical transmission case 165
AY509260.1	HIV-2 isolate MCR35, complete genome 588 1480 97% 2e- 93%
	164
L25445.1	Human immunodeficiency virus type 2 586 1414 96% 8e- 90%
	proviral envelope glycoprotein (env) gene,
	complete cds 164
AY168925.1	HIV-2 isolate MIC97 envelope glycoprotein 582 1347 92% 1e- 91%
	(env) gene, partial cds 162

AF176768.1	HIV-2 isolate SS2 from Spain envelope glycoprotein (env) gene, partial cds	582	905	65%	1e-162	89%
DQ400384.1	HIV-2 isolate CalHIV-2(BD) from India nonfunctional envelope glycoprotein (env) gene, partial sequence	580	982	69%	4e-162	88%
AJ238998.1	Human immunodeficiency virus type 2, env gene for envelope glycoprotein precursor gp130, cell line HVS T-cell CB23 (late)	580	1445	95%	4e-162	91%
AJ238996.1	Human immunodeficiency virus type 2, env-gene for envelope glycoprotein precursor gp160, cell line Molt4.c8 (late)	580	1445	95%	4e-162	91%
AJ238995.1	Human immunodeficiency virus type 2, env-gene for envelope glycoprotein precursor gp160, cell line Molt4.c8(early)	580	1445	95%	4e-162	91%
M31113.1	Human immunodeficiency virus type 2 (HIV-2), complete proviral genome	580	982	69%	4e-162	88%
M86924.1	Human immunodeficiency virus type 2 (ST/24.1C#2) envelope glycoprotein (env) gene, 5'end	580	971	69%	4e-162	88%
M30895.1	Human immunodeficiency virus type 2 (isolate GH-1) proviral DNA complete genome, clone 8	580	1329	94%	4e-162	89%
AF176770.1	HIV-2 isolate SS4 from Spain envelope glycoprotein (env) gene, partial cds	577	936	65%	5e-161	92%
AJ238997.1	Human immunodeficiency virus type 2 env gene for envelope glycoprotein precursor gp160, cell line HVS T-cell CB23 (early)	575	1440	95%	2e-160	91%
AF170044.1	HIV-2 isolate 96327 from France envelope glycoprotein (env) gene, partial cds	575	857	63%	2e-160	89%
L36874.1	HIV-2 isolate 7312a clone JK, partial genome	573	1236	95%	6e-160	89%
AF176769.1	HIV-2 isolate SS3 from Spain envelope glycoprotein (env) gene, partial cds	573	949	66%	6e-160	92%
DQ870442.1	HIV-2 clone NARI-H2-5.4 from India envelope glycoprotein (env) gene, partial cds	571	953	69%	2e-159	88%
AF170049.1	HIV-2 isolate 96203 from France envelope glycoprotein (env) gene, partial cds	571	1065	78%	2e-159	88%
DQ870450.1	HIV-2 clone NARI-H2-7.7 from India envelope glycoprotein (env) gene, partial cds	569	1373	95%	8e-159	90%
DQ870449.1	HIV-2 clone NARI-H2-7.5 from India envelope glycoprotein (env) gene, partial cds	569	1379	95%	8e-159	90%
DQ400382.1	HIV-2 isolate Cal3HIV-2(818) from India nonfunctional envelope glycoprotein (env) gene, partial sequence	569	1419	96%	8e-159	92%
AJ239000.1	Human immunodeficiency virus type 2, env-gene for envelope glycoprotein precursor gp160, cell line HVS T-cell Kesting (late)	569	1428	95%	8e-159	91%
AJ238999.1	Human immunodeficiency virus type 2, env-gene for envelope glycoprotein precursor gp160, cell line HVS T-cell Kesting (early)	569	1434	95%	8e-159	91%
AF170032.1	HIV-2 isolate 96323 from France envelope glycoprotein (env) gene, partial cds	569	999	69%	8e-159	90%
AJ001163.1	Human Immunodeficiency Virus Type 2 partial envelope sequence, isolate arm from mother in vertical transmission case	569	1010	70%	8e-159	91%

AF082339.1	HIV-2 isolate ALI from Guinea-Bissau, complete genome	569	1419	96%	8e-159	92%
L76739.1	Human immunodeficiency virus type 2 (HIV-2 ARM) proviral surface glycoprotein (gp125) gene, partial cds	569	1010	70%	8e-159	91%
U05353.1	Human immunodeficiency virus type 2 isolate HIV2CBL24 gp160 envelope (env) gene, complete cds	569	1428	95%	8e-159	91%
DQ870448.1	HIV-2 clone NARI-H2-7.2 from India envelope glycoprotein (env) gene, partial cds	564	1368	95%	4e-157	90%
AF170040.1	HIV-2 isolate 96202 from France envelope glycoprotein (env) gene, partial cds	564	1052	75%	4e-157	94%
U05359.1	Human immunodeficiency virus type 2 isolate HIV2CAM1, Guinea Bissau gp160 envelope (env) gene, complete cds	564	995	70%	4e-157	91%
DQ213034.1	HIV-2 isolate P4-2000 from Sweden envelope glycoprotein (env) gene, partial cds	562	1410	98%	1e-156	90%
DQ213033.1	HIV-2 isolate P4-1992 from Sweden envelope glycoprotein (env) gene, partial cds	558	1428	98%	2e-155	92%
DQ870471.1	HIV-2 clone NARI-H2-14.6 from India envelope glycoprotein (env) gene, partial cds	556	1408	96%	6e-155	91%
DQ870470.1	HIV-2 clone NARI-H2-14.5 from India envelope glycoprotein (env) gene, partial cds	556	1397	96%	6e-155	90%
DQ870469.1	HIV-2 clone NARI-H2-14.2 from India envelope glycoprotein (env) gene, partial cds	556	1392	96%	6e-155	90%
Z48731.1	Human immunodeficiency virus type 2 gag, pol, vif, vpx, vpr, tat, rev, nef and env genes	556	1392	97%	6e-155	90%
D00835.1	Human immunodeficiency virus 2 proviral DNA, complete genome	556	1412	97%	6e-155	90%
U05354.1	Human immunodeficiency virus type 2 isolate HIV2CAM2, Guinea Bissau gp160 envelope (env) gene, complete cds	556	1423	97%	6e-155	91%
U07106.1	Human immunodeficiency virus type 2 hiv2d766 envelope protein gp105 (env) gene, partial cds	556	1272	97%	6e-155	90%
DQ213036.1	HIV-2 isolate P4-2002 from Sweden envelope glycoprotein (env) gene, partial cds	555	1340	98%	2e-154	91%
U07104.1	Human immunodeficiency virus type 2 hiv2d1024 envelope protein gp105 (env) gene, partial cds	555	1353	96%	2e-154	90%
AY249822.1	HIV-2 subject DKN142 from Senegal envelope glycoprotein (env) gene, partial cds	551	551	39%	3e-153	87%
X05291.1	Human immunodeficiency virus type 2 ROD isolate RNA genome (HIV-2)	551	980	71%	3e-153	90%
AF176767.1	HIV-2 isolate SS1 from Spain envelope glycoprotein (env) gene, partial cds	551	953	66%	3e-153	93%
M15390.1	Human immunodeficiency virus type 2, isolate ROD, complete proviral genome	551	980	71%	3e-153	90%
DQ870477.1	HIV-2 clone NARI-H2-16.6 from India envelope glycoprotein (env) gene, partial cds	549	1379	96%	1e-152	92%

DQ870476.1	HIV-2 clone NARI-H2-16.5 from India envelope glycoprotein (env) gene, partial cds	549	1323	96%	1e-	89%
DQ870475.1	HIV-2 clone NARI-H2-16.4 from India envelope glycoprotein (env) gene, partial cds	549	1323	96%	1e-	89%
AF170045.1	HIV-2 isolate 96329 from France envelope glycoprotein (env) gene, partial cds	547	949	69%	4e-	88%
DQ213029.1	HIV-2 isolate P2-1994 from Sweden envelope glycoprotein (env) gene, partial cds	545	1288	96%	1e-	88%
J04498.1	Human immunodeficiency virus type 2, isolate SBLISY, complete genome	545	1327	96%	1e-	89%
DQ870468.1	HIV-2 clone NARI-H2-13.2 from India envelope glycoprotein (env) gene, partial cds	542	1371	95%	2e-	90%
DQ870467.1	HIV-2 clone NARI-H2-13.1 from India envelope glycoprotein (env) gene, partial cds	542	1364	95%	2e-	90%
DQ870466.1	HIV-2 clone NARI-H2-13.3 from India envelope glycoprotein (env) gene, partial cds	542	1358	95%	2e-	90%
DQ870465.1	HIV-2 clone NARI-H2-12.1 from India envelope glycoprotein (env) gene, partial cds	542	1279	96%	2e-	88%
DQ870464.1	HIV-2 clone NARI-H2-12.4 from India envelope glycoprotein (env) gene, partial cds	542	1268	96%	2e-	87%
DQ870463.1	HIV-2 clone NARI-H2-12.3 from India envelope glycoprotein (env) gene, partial cds	542	1279	96%	2e-	88%
AY249826.1	HIV-2 subject MBN5 from Senegal envelope glycoprotein (env) gene, partial cds	540	540	38%	6e-	87%
U05358.1	Human immunodeficiency virus type 2 isolate HIV2CAM6, Guinea Bissau gp160 envelope (env) gene, complete cds	540	1456	96%	6e-	92%
AF170035.1	HIV-2 isolate 96201 from France envelope glycoprotein (env) gene, partial cds	536	964	67%	8e-	90%
DQ870447.1	HIV-2 clone NARI-H2-6.1 from India envelope glycoprotein (env) gene, partial cds	532	1331	96%	1e-	89%
DQ213031.1	HIV-2 isolate P2-1998 from Sweden envelope glycoprotein (env) gene, partial cds	532	1264	96%	1e-	87%
DQ870452.1	HIV-2 clone NARI-H2-8.4 from India envelope glycoprotein (env) gene, partial cds	531	1297	96%	4e-	88%
DQ870432.1	HIV-2 clone NARI-H2-1.5 from India envelope glycoprotein (env) gene, partial cds	531	966	70%	4e-	91%
DQ870431.1	HIV-2 clone NARI-H2-1.1 from India envelope glycoprotein (env) gene, partial cds	531	966	70%	4e-	91%
DQ870430.1	HIV-2 clone NARI-H2-1.4 from India envelope glycoprotein (env) gene, partial cds	531	932	70%	4e-	89%
DQ213035.1	HIV-2 isolate P4-2001 from Sweden envelope glycoprotein (env) gene, partial cds	529	910	71%	1e-	87%
AF170037.1	HIV-2 isolate 96152 from France envelope glycoprotein (env) gene, partial cds	527	875	63%	5e-	91%
DQ870483.1	HIV-2 clone NARI-H2-18.6 from India envelope glycoprotein (env) gene, partial	525	1342	96%	2e-	89%

cds						
DQ870482.1	HIV-2 clone NARI-H2-18.1 from India envelope glycoprotein (env) gene, partial cds	525	1342	96%	2e- 145	89%
DQ870481.1	HIV-2 clone NARI-H2-18.4 from India envelope glycoprotein (env) gene, partial cds	525	1342	96%	2e- 145	89%
DQ870441.1	HIV-2 clone NARI-H2-4.1 from India glycoprotein (env) gene, partial cds	525	962	68%	2e- 145	92%
DQ870440.1	HIV-2 clone NARI-H2-4.4 from India glycoprotein (env) gene, partial cds	525	962	68%	2e- 145	92%
DQ870439.1	HIV-2 clone NARI-H2-4.3 from India glycoprotein (env) gene, partial cds	525	962	68%	2e- 145	92%
DQ400383.1	HIV-2 isolate Cal4HIV-2(889) from India nonfunctional envelope glycoprotein (env) gene, partial sequence	525	921	68%	2e- 145	89%
U22047.1	Human immunodeficiency virus type 2, complete genome	525	1384	96%	2e- 145	91%
DQ870480.1	HIV-2 clone NARI-H2-17.6 from India envelope glycoprotein (env) gene, partial cds	523	1316	96%	6e- 145	90%
DQ870479.1	HIV-2 clone NARI-H2-17.5 from India envelope glycoprotein (env) gene, partial cds	523	1316	96%	6e- 145	90%
DQ870478.1	HIV-2 clone NARI-H2-17.2 from India envelope glycoprotein (env) gene, partial cds	523	1316	96%	6e- 145	90%
U07108.1	Human immunodeficiency virus type 2 hiv2d868 envelope protein gp105 (env) gene, partial cds	523	1342	95%	6e- 145	91%
DQ870446.1	HIV-2 clone NARI-H2-6.4 from India glycoprotein (env) gene, partial cds	521	1316	95%	2e- 144	90%
DQ870445.1	HIV-2 clone NARI-H2-6.3 from India glycoprotein (env) gene, partial cds	521	1320	96%	2e- 144	89%
DQ870444.1	HIV-2 clone NARI-H2-5.2 from India glycoprotein (env) gene, partial cds	521	903	69%	2e- 144	88%

Alignments

>gb|EU580100.1| Mutant HIV-2 isolate VCP DeltaV3(6,6)+a-pl6 from USA modified envelope glycoprotein (env) gene, complete cds
Length=2172

Sort alignments for this
E value Score Perce
Query start position

Score = 1559 bits (844), Expect = 0.0
Identities = 864/874 (98%), Gaps = 0/874 (0%)
Strand=Plus/Plus

Query	336	CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG	395
Sbjct	582	CCATTGCAATACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG	641
Query	396	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATTC	455
Sbjct	642	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATACTAATTATTC	701
Query	456	AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC	515
Sbjct	702	AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC	761
Query	516	GCAATCTTCTACATGGTTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCTA	575
Sbjct	762	GCAATCTTCTACATGGTTTTGGATTTAATGGCACTAGAGCAGAAAATAGAACATATATATA	821
Query	576	TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT	635
Sbjct	822	TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT	881
Query	636	GCATTGTAAGAGGCCGGGAAATAAGGGTGCCGGCAAACCCAGGCAAGCATGGTGTGGTT	695
Sbjct	882	GCATTGTAAGAGGCCGGGAAATAAGGGTGCCGGCAAACCCAGGCAAGCATGGTGTGGTT	941
Query	696	CAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCTTGCGAAACATCCAG	755
Sbjct	942	CAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCTTGCGAAACATCCAG	1001
Query	756	ATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCAGGAAGAGGCTC	815
Sbjct	1002	ATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCAGGAAGAGGCTC	1061
Query	816	AGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTCTACTGCGACAT	875
Sbjct	1062	AGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTCTACTGCAACAT	1121
Query	876	GACTTGGTTCTCAATTGGGTAGATAACAGGACGGGTCAGAAACAGCGCAATTATGCACC	935
Sbjct	1122	GGCTTGGTTCTCAATTGGGTAGAAAACAGGACGGGTCAGAAACAGCGCAATTATGCACC	1181
Query	936	GTGCCATATAAGACAAATAATTAATACTTGGCACAGGGTAGGGAAAAACGTATATTTGCC	995
Sbjct	1182	GTGCCATATAAGGCAAATAATTAATACTTGGCACAGGGTAGGGAAAAACATATATTTGCC	1241


```

Query   996   TCCCAGGGAAGGGGAGTTGACCTGCAACTCAACAGTGACCAGCATAATTGCCAACATTGA   1055
          |||
Sbjct   1242   TCCCAGGGAAGGGGAGTTGACCTGCAACTCAACAGTGACCAGCATAATTGCCAACATTGA   1301

Query   1056   TACGGGAGATCAAACAGATATTACCTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGA   1115
          |||
Sbjct   1302   TACGGGAGATCAAACAGATATTACCTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGA   1361

Query   1116   ATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCTACATCAGTAAA   1175
          |||
Sbjct   1362   ATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCTACATCAGTAAA   1421

Query   1176   GAGATACTCCTCTGCTCACCAGAGACATACAAGA   1209
          |||
Sbjct   1422   GAGATACTCCTCTGCTCACCAGAGACATACAAGA   1455

```

Score = 579 bits (313), Expect = 1e-161
 Identities = 323/328 (98%), Gaps = 0/328 (0%)
 Strand=Plus/Plus

```

Query   1   ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA   60
          |||
Sbjct   1   ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTATACTAGCTAGTGCTTACCTAACA   60

Query   61   CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT   120
          |||
Sbjct   61   CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT   120

Query   121   CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTGTACAGTGCTTGCCAGAC   180
          |||
Sbjct   121   CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGAC   180

Query   181   AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT   240
          |||
Sbjct   181   AATGATGATTATCAGGAAATAGCTCTAAATGTAACAGAGGCTTTCGATGCATGGAATAAT   240

Query   241   ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA   300
          |||
Sbjct   241   ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA   300

Query   301   TGTGTCAAATTAACACCCTTATGTGTAG   328
          |||
Sbjct   301   TGTGTCAAATTAACACCCTTATGTGTAG   328

```

>gb|EU580103.1| Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a-p16B from USA modified
 envelope glycoprotein (env) gene, complete cds
 Length=1896

Sort alignments for this
 E value Score Percen
 Query start position

Score = 1122 bits (607), Expect = 0.0
 Identities = 639/654 (97%), Gaps = 3/654 (0%)
 Strand=Plus/Plus

```

Query   1   ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA   60
          |||
Sbjct   1   ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTATACTAGCTAGTGCTTACCTAACA   60

Query   61   CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT   120
          |||
Sbjct   61   CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT   120

Query   121   CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTGTACAGTGCTTGCCAGAC   180
          |||
Sbjct   121   CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACACACAGTGCTTGCCAGAC   180

Query   181   AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT   240
          |||
Sbjct   181   AATGATGATTATCAGGAAATAGCTCTAAATGTAACAGAGGCTTTCGATGCATGGAATAAT   240

Query   241   ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA   300

```

```

Sbjct  241  |||||
ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
Query  301  TGTGTCAAATTAACACCCTTATGTGTAGGTGCCGGCCATTGCAATACATCAGTCATCA-A 359
Sbjct  301  TGTGTCAAATTAACACCCTTATGTGTAGGTGCCGGCCATTGCAATACATCAGTCATCACA 360
Query  360  AGAGTCATGTGATAAGCACTATTGGGATGCTATGAGGTTTGTAGATACTGTGCACCACCGGG 419
Sbjct  361  A-AGTCATGTGATAAGCACTATTGGGATGCTATGAGGTTTGTAGATACTGTGCACCACCGGG 419
Query  420  TTTTGCCTACTAAGATGCAATGATATTAATTATTCAGGCTTTGCACCTAATTGCTCTAA 479
Sbjct  420  TTTTGCCTACTAAGATGCAATGATACTAATTATTCAGGCTTTGCACCTAATTGCTCTAA 479
Query  480  AGTAGTAGCTGCTACATGCACCAGAATGATGGAAACGCAATCTTCTACATGGTTTGGCTT 539
Sbjct  480  AGTAGTAGCTGCTACATGCACCAGAATGATGGAAACGCAATCTTCTACATGGTTTGGATT 539
Query  540  TAATGGCACTAGAACAGAAAATAGAACATATATCTATTGGCATGGTAAAAATAACAGAAC 599
Sbjct  540  TAATGGCACTAGAGCAGAAAATAGAACATATATATATTGGCATGGTAAAGATAACAGAAC 599
Query  600  TATTATCAGCTTAAATAACTTTTATAATCTCACTATGCATTGTAAGAG-GCCGG 652
Sbjct  600  TATTATCAGCTTAAATAACTTTTATAATCTCACTATGCATTGTAAGGGTGCCGG 653

```

Score = 898 bits (486), Expect = 0.0
Identities = 512/525 (97%), Gaps = 0/525 (0%)
Strand=Plus/Plus

```

Query  685  TGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCTTGCG 744
Sbjct  655  TGGTGTGGTTCAAAGGCAAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCTTGCG 714
Query  745  AAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 804
Sbjct  715  AAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 774
Query  805  GGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC 864
Sbjct  775  GGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC 834
Query  865  TACTGCGACATGACTTGGTTTCTCAATTGGGTAGATAACAGGACGGGTGAGAAACAGCGC 924
Sbjct  835  TACTGCAACATGGCTTGGTTTCTCAATTGGGTAGAAAACAGGACGGATCAGAAACAGCGC 894
Query  925  AATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGGCACAGGGTAGGGAAAAAC 984
Sbjct  895  AATTATGCACCGTGCCATATAAGGCAAAAAATTAATACTTGGCACAGGGTAGGGAAAAAC 954
Query  985  GTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAACAGTGACCAGCATAATT 1044
Sbjct  955  ATATATTTGCCTCCCAGGAAAGGGGTGTTTACCTGCAACTCAACAGTGACCAGCATAATT 1014
Query  1045  GCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGCAGAGGTGGCAGAACTA 1104
Sbjct  1015  GCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGCAGAGGTGGCAGAACTA 1074
Query  1105  TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1164
Sbjct  1075  TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1134
Query  1165  ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATAACAAGA 1209
Sbjct  1135  ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATAACAAGA 1179

```

>gb|EU580102.1| Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a-p16A from USA modified envelope glycoprotein gene, complete cds
Length=1896

Sort alignments for this
E value Score Percen
Query start position

Score = 1122 bits (607), Expect = 0.0
 Identities = 639/654 (97%), Gaps = 3/654 (0%)
 Strand=Plus/Plus

Query	1	ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA	60
Sbjct	1	ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTATACTAGCTAGTGCTTACCTAACA	60
Query	61	CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCCATT	120
Sbjct	61	CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCCATT	120
Query	121	CCCCTGTTTTGTGCAACCAAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCCAGAC	180
Sbjct	121	CCCCTGTTTTGTGCAACCAAAAAATAGAGATACTTGGGGAACACACAGTGCTTGCCAGAC	180
Query	181	AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTTCGATGCATGGGATAAT	240
Sbjct	181	AATGATGATTATCAGGAAATAGCTCTAAATGTAACAGAGGCTTTTCGATGCATGGAATAAT	240
Query	241	ACAGTAACAGAACAAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA	300
Sbjct	241	ACAGTAACAGAACAAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA	300
Query	301	TGTGTCAAATTAACACCCTTATGTGTAGGTGCCGGCCATTGCAATACATCAGTCATCA-A	359
Sbjct	301	TGTGTCAAATTAACACCCTTATGTGTAGGTGCCGGCCATTGCAATACATCAGTCATCACA	360
Query	360	AGAGTCATGTGATAAGCACTATTGGGATGCTATGAGGTTTAGATACTGTGCACCACCGGG	419
Sbjct	361	A-AGTCATGTGATAAGCACTATTGGGATGCTATGAGGTTTAGATACTGTGCACCACCGGG	419
Query	420	TTTTGCCCTACTAAGATGCAATGATATTAATTATTCAGGCTTTGCACCTAATTGCTCTAA	479
Sbjct	420	TTTTGCCCTACTAAGATGCAATGATACTAATTATTCAGGCTTTGCACCTAATTGCTCTAA	479
Query	480	AGTAGTAGCTGCTACATGCACCAGAATGATGGAAACGCAATCTTCTACATGGTTTGGCTT	539
Sbjct	480	AGTAGTAGCTGCTACATGCACCAGAATGATGGAAACGCAATCTTCTACATGGTTTGGATT	539
Query	540	TAATGGCACTAGAACAGAAAAATAGAACATATATCTATTGGCATGGTAAAAATAACAGAAC	599
Sbjct	540	TAATGGCACTAGAGCAGAAAAATAGAACATATATATATTGGCATGGTAAAGATAACAGAAC	599
Query	600	TATTATCAGCTTAAATAACTTTTATAATCTCACTATGCATTGTAAGAG-GCCGG	652
Sbjct	600	TATTATCAGCTTAAATAACTTTTATAATCTCACTATGCATTGTAAGGGTGCCGG	653

Score = 898 bits (486), Expect = 0.0
 Identities = 512/525 (97%), Gaps = 0/525 (0%)
 Strand=Plus/Plus

Query	685	TGGTGTITGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCTTGCG	744
Sbjct	655	TGGTGTITGGTTCAAAGGCAAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCTTGCG	714
Query	745	AAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA	804
Sbjct	715	AAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA	774
Query	805	GGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC	864
Sbjct	775	GGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC	834
Query	865	TACTGCGACATGACTTGGTTTCTCAATTGGGTAGATAACAGGACGGGTGAGAAACAGCGC	924
Sbjct	835	TACTGCAACATGGCTTGGTTTCTCAATTGGGTAGAAAACAGGACGGATCAGAAACAGCGC	894
Query	925	AATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGGCACAGGGTAGGGAAAAAC	984
Sbjct	895	AATTATGCACCGTGCCATATAAGGCAAAAAATTAATACTTGGCACAGGGTAGGGAAAAAC	954
Query	985	GTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAACAGTGACCAGCATAATT	1044

```

Sbjct  955  ATATATTTGCCTCCCAGGGAAGGAGTGTTTACCTGCAACTCAACAGTGACCAGCATAATT 1014
Query  1045  GCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGAGAGGTGGCAGAACTA 1104
          |||
Sbjct  1015  GCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGAGAGGTGGCAGAACTA 1074
Query  1105  TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1164
          |||
Sbjct  1075  TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1134
Query  1165  ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1209
          |||
Sbjct  1135  ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1179

```

>gb|EU580099.1| HIV-2 isolate vcp from USA envelope glycoprotein (env) gene,
complete cds
Length=2220

Sort alignments for this
E value Score Perce
Query start position

Score = 981 bits (531), Expect = 0.0
Identities = 537/540 (99%), Gaps = 0/540 (0%)
Strand=Plus/Plus

```

Query  670  AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTG 729
          |||
Sbjct  964  AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTG 1023
Query  730  AAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATT 789
          |||
Sbjct  1024  AAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATT 1083
Query  790  AAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATAACATGTGGACTAACTGC 849
          |||
Sbjct  1084  AAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATAACATGTGGACTAACTGC 1143
Query  850  AGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCTCAATTGGGTAGATAACAGGACG 909
          |||
Sbjct  1144  AGAGGGGAATTTCTCTACTGCAACATGACTTGGTTCTCAATTGGGTAGAAAACAGGACG 1203
Query  910  GGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGGCAC 969
          |||
Sbjct  1204  GGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGGCAAATAATTAATACTTGGCAC 1263
Query  970  AGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAACA 1029
          |||
Sbjct  1264  AGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAACA 1323
Query  1030  GTGACCAGCATAATTGCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGCA 1089
          |||
Sbjct  1324  GTGACCAGCATAATTGCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGCA 1383
Query  1090  GAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCA 1149
          |||
Sbjct  1384  GAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCA 1443
Query  1150  ATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1209
          |||
Sbjct  1444  ATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1503

```

Score = 584 bits (316), Expect = 3e-163
Identities = 324/328 (98%), Gaps = 0/328 (0%)
Strand=Plus/Plus

```

Query  1  ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
          |||
Sbjct  1  ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
Query  61  CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCCATT 120
          |||
Sbjct  61  CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCCATT 120

```

```

Query 121 CCCCTGTTTTGTGCAACCAAAAAATAGAGATACTTGGGGAACGTGTACAGTGCTTGCCAGAC 180
          |||
Sbjct 121 CCCCTGTTTTGTGCAACCAAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGAC 180

Query 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT 240
          |||
Sbjct 181 AATGATGATTATCAGGAAATAGCTCTAAATGTAACAGAGGCTTTCGATGCATGGAATAAT 240

Query 241 ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
          |||
Sbjct 241 ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300

Query 301 TGTGTCAAATTAACACCCTTATGTGTAG 328
          |||
Sbjct 301 TGTGTCAAATTAACACCCTTATGTGTAG 328

```

Score = 584 bits (316), Expect = 3e-163
 Identities = 322/325 (99%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

```

Query 336 CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395
          |||
Sbjct 582 CCATTGCAATACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 641

Query 396 GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATTC 455
          |||
Sbjct 642 GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATACTAATTATTC 701

Query 456 AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC 515
          |||
Sbjct 702 AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC 761

Query 516 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCTA 575
          |||
Sbjct 762 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAGCAGAAAATAGAACATATATCTA 821

Query 576 TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT 635
          |||
Sbjct 822 TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT 881

Query 636 GCATTGTAAGAGGCCGGGAAATAAG 660
          |||
Sbjct 882 GCATTGTAAGAGGCCGGGAAATAAG 906

```

>gb|EU580101.1| Mutant HIV-2 isolate VCP DeltaV3(1,1)+a-p36 from USA modified
 envelope glycoprotein (env) gene, complete cds
 Length=2142

Sort alignments for this
 E value Score Perce
 Query start position

Score = 920 bits (498), Expect = 0.0
 Identities = 516/525 (98%), Gaps = 0/525 (0%)
 Strand=Plus/Plus

```

Query 685 TGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCTTGCG 744
          |||
Sbjct 901 TGGTGTGGTTCAAAGGCAAATGGAAGAAAGCCATGCAGGAGGTGAAGGAGACCCTTGCG 960

Query 745 AAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 804
          |||
Sbjct 961 AAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 1020

Query 805 GGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC 864
          |||
Sbjct 1021 GGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC 1080

Query 865 TACTGCGACATGACTTGGTTTCTCAATTGGGTAGATAACAGGACGGGTGAGAAACAGCGC 924
          |||
Sbjct 1081 TACTGCAACATGGCTTGGTTTCTCAATTGGGTAGAAAACAGGACGGGTGAGAAACAGCGC 1140

Query 925 AATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGGCACAGGGTAGGGAAAAAC 984
          |||

```

```
Sbjct 1141 AATTATGCACCGTGCCATATAAGGCAAATAATTAATACTTGGCACAGGGTAGGGAAAAAC 1200
Query 985 GTATATTTGCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAACAGTGACCAGCATAATT 1044
          |||
Sbjct 1201 ATATATTTGCTCCCAGGGAAGGGGTGTTTACCTGCAACTCAACAGTGACCAGCATAATT 1260
Query 1045 GCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGCAGAGGTGGCAGAACTA 1104
          |||
Sbjct 1261 GCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGCAGAGGTGGCAGAACTA 1320
Query 1105 TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1164
          |||
Sbjct 1321 TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1380
Query 1165 ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1209
          |||
Sbjct 1381 ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1425
```

Score = 579 bits (313), Expect = 1e-161
Identities = 323/328 (98%), Gaps = 0/328 (0%)
Strand=Plus/Plus

```
Query 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
          |||
Sbjct 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTATACTAGCTAGTGCTTACCTAACA 60
Query 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCCATT 120
          |||
Sbjct 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCCATT 120
Query 121 CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCCAGAC 180
          |||
Sbjct 121 CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGAC 180
Query 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTTCGATGCATGGGATAAT 240
          |||
Sbjct 181 AATGATGATTATCAGGAAATAGCTCTAAATGTAACAGAGGCTTTTCGATGCATGGAATAAT 240
Query 241 ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
          |||
Sbjct 241 ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
Query 301 TGTGTCAAATTAACACCCTTATGTGTAG 328
          |||
Sbjct 301 TGTGTCAAATTAACACCCTTATGTGTAG 328
```

Score = 536 bits (290), Expect = 8e-149
Identities = 310/319 (97%), Gaps = 3/319 (0%)
Strand=Plus/Plus

```
Query 336 CCATTGCAATACATCAGTCATCA-AAGAGTCATGTGATAAGCACTATTGGGATGCTATGA 394
          |||
Sbjct 582 CCATTGCAATACATCAGTCATCACA-AGTCATGTGATAAGCACTATTGGGATGCTATGA 640
Query 395 GGTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATT 454
          |||
Sbjct 641 GGTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATACTAATTATT 700
Query 455 CAGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAA 514
          |||
Sbjct 701 CAGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAA 760
Query 515 CGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCT 574
          |||
Sbjct 761 CGCAATCTTCTACATGGTTTGGATTAAATGGCACTAGAGCAGAAAATAGAACATATATAT 820
Query 575 ATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTA 634
          |||
Sbjct 821 ATTGGCATGGTAAAGATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTA 880
Query 635 TGCATTGTAAGAG-GCCGG 652
          |||
Sbjct 881 TGCATTGTAAGGGTGCCGG 899
```

>gb|J03654.1|HIV2NIHZ Human immunodeficiency virus type 2, isolate HIV2FG
Length=9431

Sort alignments for this
E value Score Percen
Query start position

Score = 893 bits (483), Expect = 0.0
Identities = 522/541 (96%), Gaps = 2/541 (0%)
Strand=Plus/Plus

Query	670	AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTG	729
Sbjct	7105	AAACCCAGGCAAGCATGGTGTGGTTCAAGGCGAATGGAAGGAAGCCATGCAGGAGGTG	7164
Query	730	AAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATT	789
Sbjct	7165	AAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATT	7224
Query	790	AAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGC	849
Sbjct	7225	AAATTTAAAGCACCAGGGAGAGGCTCAGACCCAGAAGTAACATACATGTGGACTAACTGC	7284
Query	850	AGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGGACG	909
Sbjct	7285	AGAGGAGAATCTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTAGAGAACAGGACG	7344
Query	910	GGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGGCAC	969
Sbjct	7345	GGTCAGAAACAGCGCAATTATGCACCGTGCCGTATAAGGCAAATAATTAATACCTGGCAC	7404
Query	970	AGGGTAGGGAAAAA-CGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	1028
Sbjct	7405	AGGGTAGGGAAAAATC-TATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	7463
Query	1029	AGTGACCAGCATAATTGCCAACATTGATACGGGAGATCAAACAGATATTACCTTTAGTGC	1088
Sbjct	7464	GGTGACCAGCATAATTGCCAACATTGATGCGGGAGATCAAACAAATATTACCTTTAGTGC	7523
Query	1089	AGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACC	1148
Sbjct	7524	AGAGGCGGCAGAACTATACCGATTGGAATTGGGGGATTACAAATTAGTAGAAATCACACC	7583
Query	1149	AATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAG	1208
Sbjct	7584	AATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAG	7643
Query	1209	A 1209	
Sbjct	7644	A 7644	

Score = 551 bits (298), Expect = 3e-153
Identities = 318/328 (96%), Gaps = 0/328 (0%)
Strand=Plus/Plus

Query	1	ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA	60
Sbjct	6139	ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAATA	6198
Query	61	CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT	120
Sbjct	6199	CATTGCAAGCAATTTGTGACTGTTTTCTACGGCATAACCCGCGTGGAGGAATGCATCCATT	6258
Query	121	CCCCTGTTTTGTGCAACCAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCCAGAC	180
Sbjct	6259	CCCCTGTTTTGTGCAACCAAAATAGAGATACTTGGGGAACAATACAGTGCTTACCAGAC	6318
Query	181	AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTTCGATGCATGGGATAAT	240
Sbjct	6319	AATGATGATTATCAGGAAATAACTCTAAATGTGACAGAGGCTTTTCGATGCATGGAATAAT	6378
Query	241	ACAGTAACAGAACAAGCAGTGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA	300
Sbjct	6379	ACAGTAACAGAACAAGCAGTAGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA	6438

```

Query   301      TGTGTCAAATTAACACCCTTATGTGTAG   328
          |||
Sbjct   6439      TGTGTCAAATTAACACCCTTATGTGTAG   6466

```

Score = 551 bits (298), Expect = 3e-153
 Identities = 316/325 (97%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

```

Query   336      CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG   395
          |||
Sbjct   6717      CCATTGCAACACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG   6776

Query   396      GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATTC   455
          |||
Sbjct   6777      GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATACCAATTATTC   6836

Query   456      AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC   515
          |||
Sbjct   6837      AGGCTTTGCACCTAACTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC   6896

Query   516      GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCTA   575
          |||
Sbjct   6897      GCAAACTTCTACATGGTTTGGCTTTAATGGCACTAGAGCAGAAAATAGAACATATATCTA   6956

Query   576      TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT   635
          |||
Sbjct   6957      TTGGCATGGTAAAGATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT   7016

Query   636      GCATTGTAAGAGGCCGGGAAATAAG   660
          |||
Sbjct   7017      GCATTGTAAGAGGCCGGGAAATAAG   7041

```

>gb|U05355.1|HIV2U05355 Human immunodeficiency virus type 2 isolate HIV2CAM3, Gu
 Bissau gp160 envelope (env) gene, complete cds
 Length=2583

Sort alignments for this
 E value Score Perce
 Query start position

Score = 632 bits (342), Expect = 1e-177
 Identities = 487/554 (87%), Gaps = 22/554 (3%)
 Strand=Plus/Plus

```

Query   669      CAA-ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGG   727
          |||
Sbjct   995      CAAGACCTAGGCAAGCATGGTGTGGTTCAAAGGCAAATGGAAGGAAGCCATGCAGGAGG   1054

Query   728      TGAAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAA-C-AGGAGCCGCACAGAGAA   785
          |||
Sbjct   1055      TAAAGGAAACCCTTGCCAAACATCCCAGGTATAAA-GGAACCAATGA----CACAAAGAA   1109

Query   786      TATTAAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATAACATGTGGACTAA   845
          |||
Sbjct   1110      GATTAACCTTTGCAGCACCAGGAAGAGGCTCAGACCCAGAGGTGGCATAACATGTGGACTAA   1169

Query   846      CTGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAG   905
          |||
Sbjct   1170      CTGCAGAGGGGAATTTCTCTACTGCAACATGACTTGGTTCCTTAATTGGGTAGAGAACAG   1229

Query   906      GAC-G-G-GTCA-GAAACAGCGCAATTATGCACCGTGCCATATAAGACAAATAATTAATA   961
          |||
Sbjct   1230      AACTGAGAAT-AGGACATGGCACAATTATGTGCCATGCCATATAAGGCAAATAATTAACA   1288

Query   962      CTTGGCACAGGGTAGGGAAAAAC-GTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGC   1020
          |||
Sbjct   1289      CCTGGCATAAGGTA-GGAAAAATGTATATTTGCCTCCCAGGGAAGGGGAGTTAACCTGC   1347

Query   1021      AACTCAACAGTGACCAGCATAATTGCCAACATTGATACG-GGA-G-A--TCAAACAGATA   1075
          |||
Sbjct   1348      AACTCAACAGTGACCAGCATAATTGCTAACATTGA--CGTGGAAGCAAATCAGACAAATA   1405

Query   1076      TTACCTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAG   1135

```



```

Sbjct  1406  |||||
TTACCTTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAGTTGGGAGATTATAAATTGG 1465
Query  1136  TAGAAATCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACC 1195
Sbjct  1466  TAGAAATAACACCAATTGGCTTCGCACCTACATCAGAAAAGCGATACTCCTCTGCTCACA 1525
Query  1196  AGAGACATACAAGA 1209
Sbjct  1526  AGAGACATACAAGA 1539

```

Score = 438 bits (237), Expect = 2e-119
 Identities = 297/326 (91%), Gaps = 4/326 (1%)
 Strand=Plus/Plus

```

Query  336  CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395
Sbjct  612  CCATTGCAACACATCAGTCATCACAGAATCATGTGATAAGCACTATTGGGATGCTATAAG 671
Query  396  GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATTC 455
Sbjct  672  GTTTAGATACTGTGCACCACCGGGTTATGCCCTGCTAAGGTGCAATGATACCAATTATTC 731
Query  456  AGGCTTTGCA-CCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAA 514
Sbjct  732  AGGCTTTG-AGCCCAATTGCTCTAAAGTAGTAGCTACTACATGCACCAGGATGATGGAAA 790
Query  515  CGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCT 574
Sbjct  791  CACAACTTCTACATGGTTTGGCTTTAATGGCACAAGAGCAGAGAATAGAACATATATCT 850
Query  575  ATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAC-T 633
Sbjct  851  ATTGGCATGGTAGAGATAACAGAACTATCATCAGCTTAAACAAATATTATAATCTCTCCT 910
Query  634  ATGCATTGTAAGAGGCCGGGAAATAA 659
Sbjct  911  -TGCATTGTAAGAGGCCAGGAAATAA 935

```

Score = 405 bits (219), Expect = 2e-109
 Identities = 285/317 (89%), Gaps = 3/317 (0%)
 Strand=Plus/Plus

```

Query  15  GAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACACATTGCAAGC-A-A 72
Sbjct  15  GAATCAGCTGCTTATTGCTATTTTACTAGCTAGTGCCTACTTAATATATTGCAGGCAACA 74
Query  73  -TTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATTCCCCTGTTTTG 131
Sbjct  75  GTATGTAAGTGTATTTTATGGCATAACCCGCGTGGAGAAATGCAACCATTCCCCTCTTTTG 134
Query  132  TGCAACCAAAAATAGAGATACTTGGGGAAGTGTACAGTGCTTGCCAGACAATGATGATTA 191
Sbjct  135  TGCAACCAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGACAATGATGATTA 194
Query  192  TCAGGAAATAGCTTTAAATGTAACAGAGGCTTTTCGATGCATGGGATAATACAGTAACAGA 251
Sbjct  195  TCAGGAAATATCCTTGAATGTGACAGAGGCTTTTGATGCATGGAATAATACAGTAACAGA 254
Query  252  ACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCATGTGTCAAATT 311
Sbjct  255  ACAAGCAATAGAAGATGTCTGGAGTCTATTCGAGACATCAATAAAGCCATGTGTCAAGTT 314
Query  312  AACACCCTTATGTGTAG 328
Sbjct  315  AACACCCTTATGTGTAG 331

```

>gb|U05351.1|HIV2U05351 Human immunodeficiency virus type 2 isolate HIV2CBL22 gp
 (env) gene, complete cds
 Length=2556

Sort alignments for this
 E value Score Percen

Score = 617 bits (334), Expect = 3e-173
Identities = 469/532 (88%), Gaps = 18/532 (3%)
Strand=Plus/Plus

Query	670	AAACCCAGGCAAGCATGGTGTGGTTTCAAAGGCGA-ATGGAAGGAAGCCATGCAGGAGGT	728
Sbjct	985	AAACCCAGACAAGCATGGTGCTGGTTCCAAGGC-AGATGGAAGGAAGCCATGCAGGAGGT	1043
Query	729	GAAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAA-CAGGAGCCGCACAGAGAATA	787
Sbjct	1044	GAAGCAAACCCTTGCGAAACATCCCAGGTATAAA-GGAACCA--A-CAATACAGAGAGTA	1099
Query	788	TTAAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAG-CATACATGTGGACTAAC	846
Sbjct	1100	TTACCTTTACAGCACCAGGGAGAGGCTCTGACCCAGAAG-TGACATACATGTGGACTAAC	1158
Query	847	TGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGG	906
Sbjct	1159	TGCAGAGGAGAATTCTCTATTGCAACATGACTTGGTTCCTCAATTGGGTAGAAAATAAG	1218
Query	907	ACGGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAA-GACAAATAATTAATACTTG	965
Sbjct	1219	ACGGGTCAGACACAGCGCAACTATGTGCCGTGCCATATAAAG-CAAATAATTAATAACCTG	1277
Query	966	GCACAGGGTAGGGAAAAACGTATATTTGCCTCCAGGGAAGGGGAGTTGACCTGCAACTC	1025
Sbjct	1278	GCATAAGGTAGGGAAAAATGTATATTTGCCTCCTAGGGAAGGAGAGTTGTCCTGCAACTC	1337
Query	1026	AACAGTGACCAGCATAATTGCCAACATTGAT--ACG-GG-AGATCAAACAGATATTACCT	1081
Sbjct	1338	AACAGTGACCAGCATACTCGCTAACATTGATGTAAATGGTA-ATCAAACAAATATTACCT	1396
Query	1082	TTAGTGACAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAA	1141
Sbjct	1397	TTAGTGACAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTATAAATTAGTAGAAA	1456
Query	1142	TCACACCAATTGGCTTCGCACCTACATCAGT-AAAGAGATACTCCTCTGCTC	1192
Sbjct	1457	TAACACCAATTGGCTTCGCACCTACAACAGAGAAA-AGATACTCCTCTACTC	1507

Score = 416 bits (225), Expect = 1e-112
Identities = 294/327 (89%), Gaps = 6/327 (1%)
Strand=Plus/Plus

Query	336	CCATTGCAATACATCAGTCATCAAAGAGTCA	TGTGATAAGCACTATTGGGATGCTATGAG	395
Sbjct	597	CCATTGCAACACGTCAGTCATCAAAGGGTCA	TGTGACAAGCACTATTGGGATACTATGAG	656
Query	396	GTTTAGATACTGTGCACCACCGGGTTT	TGCCCTACTAAGATGCAATGATATTAATTATTC	455
Sbjct	657	GTTTAGATACTGTGCACCACCGGGTTT	TGCCTTGCTAAGATGCAATGATACCAATTATTC	716
Query	456	AGGCTTTGCA-CCTAATTGCTCTAAAGTAG	TAGCTGCTACATGCACCAGAATGATGGAAA	514
Sbjct	717	AGGCTTTG-AGCCCAATTGCTCTAAAGTAG	TAGCTTCTACATGCACAAGGATGATGGAAA	775
Query	515	CGCAATCTTCTACATGGTTTGGCTTTAAT	TGGCACTAGAACAGAAAATAGAACATATATCT	574
Sbjct	776	CGCAAACCTTCTACTTGGTTTGGCTTTAAT	TGGCACTAGAGCAGAAAATAGAACATATATGT	835
Query	575	ATTGGCATGGTAAAA-ATAACAGAACTATT	ATCAGCTTAAATAA-CTTTTATAATCTCAC	632
Sbjct	836	ATTGGCATGG-AAGGGACAATAGAACTATT	ATCAGCTTGAACAAACATT-ATAATCTCAC	893
Query	633	TATGCATTGTAAGAGGCCGGGAAATAA	659	
Sbjct	894	CATACATTGTAAGAGGCCAGGAAATAA	920	

Score = 399 bits (216), Expect = 1e-107
Identities = 288/322 (89%), Gaps = 8/322 (2%)
Strand=Plus/Plus

```

Query 11  GTAAGAA-TCAACTGC-TGATTGCTATTGTACTAGCTAGTGCTTACCTAACACATTGCAA 68
          ||||| || ||| ||||| || ||||| ||| | ||| ||||| ||||| ||| | ||||| ||
Sbjct 8    GTAA-AATTCAAGCTGCTTG-TTGCCATTTTGCTAACTAGTGCTTGCTTAGTATATTGCAC 65

Query 69  GCAATTTGTGACTGTTTTCTATGGCA-TACCCGCGTGGAGGAATGCATCCATTCCCCTGT 127
          ||||| ||||| ||||| ||||| ||| | ||||| ||||| ||||| ||||| ||||| ||
Sbjct 66  CCAATATGTGACTGTTTTCTATGG-AGTACCCGCGTGGAGGAATGCATCCATCCCCCTCT 124

Query 128  TTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCCAGACAATGATG 187
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 125  TTTGTGCAACCAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGACAATGATG 184

Query 188  ATTATCAGGAAATAGCTTTTAAATGTAACAGAGGC-TTTCGATGCATGGGATAATACAGTA 246
          ||||| || || ||| ||||| ||||| ||||| ||| ||| ||||| ||||| ||||| ||
Sbjct 185  ATTATCAAGAGCTAACTTTTAAATGTAACAGAGGCCTTT-GATGCATGGGATAATACAGTA 243

Query 247  ACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCATGTGTC 306
          ||||| ||||| || || ||||| ||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 244  ACAGAACAAGCAATAGAAGATGTCTGGCATCTATTTGAGACATCAATAAAACCATGTGTC 303

Query 307  AAATTAACACCCTTATGTGTAG 328
          ||||| ||||| ||||| |||||
Sbjct 304  AAATTAACACCTTTATGTGTAG 325

```

>gb|AF170050.1|AF170050 HIV-2 isolate 96325 from France envelope glycoprotein (e partial cds
Length=1688

Sort alignments for this
E value Score Percen
Query start position

Score = 614 bits (332), Expect = 4e-172
Identities = 469/532 (88%), Gaps = 24/532 (4%)
Strand=Plus/Plus

```

Query 672  ACCCAGGCAAGCATGGTGTGTTGGTTCAAAGGCGAATGGAAG-GAAGCCATGCAGGAGGTGA 730
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 293  ACCTAGGCAAGCATGGTGTGTTGGTTCAAAGGCGAGTGG-AGAGAAGCCATGCGGGAGGTGA 351

Query 731  AGGAGACCCTTGCGA-AACATCCCAGATATAAAGGGGAA-CAGGAGCCGCACAGA-GAATA 787
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 352  AGGAGACCCTTGC-ARAMCATCCCAGGTATAAA-AGAATCA--A-TGGCACA-AMCAATA 405

Query 788  TTAAATTT--AAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATAACATGTGGACTAA 845
          ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 406  TTAAATTTGCAAA--ACCAGGAAGTGGCTCAGACCCAGAAGTGGCATAACATGTGGACTAA 463

Query 846  CTGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAG 905
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 464  CTGCAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTAGAGAACAG 523

Query 906  GACGGGTGAGAAACAGCGCAATTATGCACCGTGCCATATAA-GACAAATAATTAATACTT 964
          ||| ||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 524  TACGAATCAGACACAACACAATTATGCGCCGTGCCATATAAAG-CAAATAATTAATACCT 582

Query 965  GGCACAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACT 1024
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 583  GGCACAAGGTAGGGAAAAATGTATATTTGCCTCCTAGGGAAGGAGAGTTAACCTGCAACT 642

Query 1025  CAACAGTGACCAGCATAATTGCCAACATTGA--TACGGGAGATCA--A-ACAGATATTAC 1079
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 643  CAACAGTGACCAGCATAATTGCTAACATTGACGTA-GGCA-ATAACRAGACAAATATTAC 700

Query 1080  CTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGA 1139
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 701  CTTTAGTGCAGAGGTGGCAGAACTGTACCGATTGGAATTGGGAGATTATAAATTAATAGA 760

Query 1140  AATCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCT 1191
          | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 761  AGTGACACCAATTGGCTTCGCACCTACATCAGAAAAAAGATACTCCTCTGCT 812

```

Score = 270 bits (146), Expect = 9e-69
Identities = 204/232 (87%), Gaps = 4/232 (1%)

Strand=Plus/Plus

```

Query   431  TAAGATGCAATGATATTAATTATTCAGGCTTTGCA-CCTAATTGCTCTAAAGTAGTAGCT  489
          |||||
Sbjct   1    TAAGATGCAATGATACCAATTATTCAGGCTTTG-AGCCCAATTGTTCTAAAGTAGTAGCT  59

Query   490  GCTACATGCACCAGAATGATGGAAACGCAATCTTCTACATGGTTTGGCTTTAATGGCACT  549
          |||||
Sbjct   60  GCTACATGCACAAGAATGATGGAGACGCAAACCTCCACTTGGTTTGGCTTTAATGGCACT  119

Query   550  AGAACAGAAAATAGAACATATATCTATTGGCATGGTAAAAATAACAGAACTATTATCAGC  609
          |||||
Sbjct   120  AGGGCAGTAAATAGAACATTTATCTATTGGCATGGCAGGGATAATAGGACTATTATCAGC  179

Query   610  TTAAATAA-CTTTTATAATCTCACTATGCATTGTAAGAGGCCGGGAAATAAG  660
          |||||
Sbjct   180  TTAAACAAGC-ATTATAATCTCACTATGCATTGTAAGAGGCCAGGAAACAAG  230

```

>gb|AF170042.1|AF170042 HIV-2 isolate 96308 from France envelope glycoprotein (e partial cds
Length=1779

Sort alignments for this
E value Score Percen
Query start position

Score = 612 bits (331), Expect = 1e-171
Identities = 476/544 (87%), Gaps = 18/544 (3%)
Strand=Plus/Plus

```

Query   678  GCAAGCATGGTGTGTTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGAC  737
          |||||
Sbjct   346  GCAAGCATGGTGTGTTGGTTCAAAGGCAAATGGAAGGAAGCCATGCAGGAGGTGAAACAGAC  405

Query   738  CCTTGCGAAACATCCCAGATATAAAGGGAA-CAGGAGCCGCACAGAGAATATTAAATTTA  796
          |||||
Sbjct   406  CCTTGCGAAACATCCCAGGTACAAA-GGAACCA--A-TAAAACCGAGAATATTACCTTTA  461

Query   797  AAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATAACATGTGGACTAACTGCAGAGGGG  856
          |||||
Sbjct   462  CAGCACCAGGAAAAGGCTCAGACCCAGAAGTAGCATAACATGTGGACTAACTGTAGAGGAG  521

Query   857  AATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAG---GAC-GG--  910
          |||||
Sbjct   522  AATTTTGTACTGCAACATGACTTGGTTCCTCAATTGGATAGAAAACAGAACTACTGGAA  581

Query   911  GTCAGAAACAGCGCAATTATGCACCGTGCCATAT-AAGACAAATAATTAATACTTGGCAC  969
          |||||
Sbjct   582  ATCATAACATGGCACAATTATGTACCGTGCCATATAAAG-CAAATTATTAATACCTGGCAT  640

Query   970  AGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAACA  1029
          |||||
Sbjct   641  AAAGTAGGGAAAAATGTATATTTGCCTCCCAGGGAAGGGGAATTAACCTGCAACTCAACA  700

Query   1030  GTGACCAGCATAATTGCCAACATTGATAC-GG-GAG-ATCAAACAGATATTACCTTTAGT  1086
          |||||
Sbjct   701  GTGAGCAGCATAATTGCCAACATTGATACAGGTGGGAATCAAACAAATATTACCTTTAGT  760

Query   1087  GCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACA  1146
          |||||
Sbjct   761  GCAGAGGTGGCAGAACTGTACCGATTGGAATTGGGAGATTATAAATTAGTAGAAATAACA  820

Query   1147  CCAATTGGCTTCGCACCTACATCA-GTAAAGAGATACTCCTCTGCTCACCAGAGACATAC  1205
          |||||
Sbjct   821  CCAATTGGCTTCGCACCTACAG-ATGTAAAGAGATACTCCTCTACTCATGAGAGACATAA  879

Query   1206  AAGA 1209
          ||||
Sbjct   880  AAGA 883

```

Score = 379 bits (205), Expect = 1e-101
Identities = 255/279 (91%), Gaps = 3/279 (1%)
Strand=Plus/Plus

```
>gb|U05352.1|HIV2U05352 Human immunodeficiency virus type 2 isolate HIV2CBL23 gp
(env) gene, complete cds
Length=2580
```

```
Sort alignments for this
E value  Score  Percen
Query start position
```

Score = 599 bits (324), Expect = 1e-167
Identities = 464/528 (87%), Gaps = 23/528 (4%)
Strand=Plus/Plus

Query	672	ACCCAGGCAAGCATGGTGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAA	731
Sbjct	987	ACCCAGACAAGCATGGTGTGTGGTTCAAAGGTGAATGGAAGGGAGCCATGCAGGAGGTGAA	1046
Query	732	GGAGACCCCTTGCGAAACATCCCAGATATAAAGGGAA-C-AGGAGCCGCACAGAGAATATT	789
Sbjct	1047	GGAAACCCCTTGCAAAACATCCCAGGTATAAA-GGAACCAATGA----AACAAAGAATATT	1101
Query	790	AAATTTAAAGCACCAGG-AAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTG	848
Sbjct	1102	AACTTTACAGCACCAGGAAAG-GGCTCAGACCCAGAGGTGGCATACATGTGGACTAACTG	1160
Query	849	CAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGGAC	908
Sbjct	1161	CAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGATAG--AA-A--A-	1214
Query	909	GGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGGCA	968
Sbjct	1215	---TAAGACACACCGCAATTATGTACCGTGCCATATAAGACAAATAATTAACACCTGGCA	1271
Query	969	CAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	1028
Sbjct	1272	TAAGGTAGGGAAAAATGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	1331
Query	1029	AGTGACCAGCATAATTGCCAACATTGATACG---GGAGATCAA-ACAGATATTACCTTTA	1084
Sbjct	1332	AGTAAC TAGCATAATTGCTAACATTGATGCAAATGGAAAT-AATACAGATATTACCTTTA	1390
Query	1085	GTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCA	1144
Sbjct	1391	GTGCAGAGGTGGCAGAACTATACCGATTAGAGTTGGGAGATTATAAATTGGTAGAAATAA	1450
Query	1145	CACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC	1192
Sbjct	1451	CACCAATTGGCTTCGCACCTACAGCAGAAAAAAGATACTCCTCTACTC	1498

Score = 479 bits (259), Expect = 1e-131
Identities = 303/325 (93%), Gaps = 0/325 (0%)
Strand=Plus/Plus

Query 336 CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395

```

Sbjct  597  CCATTGCAACACATCGGTCATCACAGAGTCATGTGACAAGCACTATTGGGATGCTATGAG  656
Query   396  GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATTC  455
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  657  GTTTAAATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATACCAATTATTC  716
Query   456  AGGCTTTGACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC  515
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  717  AGGCTTTGCGCCCAATTGCTCTAAGGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC  776
Query   516  GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCTA  575
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  777  GCAAACTTCTACATGGTTTGGCTTTAATGGCACTAGAGCAGAAAATAGAACATTTATCTA  836
Query   576  TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT  635
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  837  TTGGCATGGTAGGGATAACAGAACTATCATCAGCTTAAACAAATATTATAATCTCACTAT  896
Query   636  GCATTGTAAGAGGCCGGGAAATAAG  660
        ||||| ||||| ||||| ||||| |||||
Sbjct  897  ACATTGTAAGAGGCCAGGAAATAAG  921

```

Score = 418 bits (226), Expect = 3e-113
 Identities = 297/331 (89%), Gaps = 6/331 (1%)
 Strand=Plus/Plus

```

Query   1  ATGAAGGGTAGTAAG-AATCAACTGC-TGATTGCTATTGTACTAGCTAGTGCTTACCTAA  58
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1  ATGATGGGTGGT-AGAAATCAGCTGCTTG-TTGCCATTTTGTAGCTAGTACTTGCTTGA  58
Query   59  CACATTGCAAGCAATT-TGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCC  117
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   59  TATATTGC-ACCAATTATGTGACTGTTTTCTATGGCATAACCCGCGTGGAGAAATGCATCC  117
Query   118  ATTCCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCCA  177
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   118  ATTCCCCTCTTTTGTGCAACCAAGAATAGGGATACTTGGGGAACCATACAGTGCTTGCCA  177
Query   178  GACAATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGAT  237
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   178  GACAATGATGATTATCAGGAGATAACTTTGAATGTGACAGAGGCTTTCGATGCATGGGAT  237
Query   238  AATACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAA  297
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   238  AATACAGTAACAGAACAAGCAATAGAAGATGTCTGGAATCTATTTGAGACATCAATAAAA  297
Query   298  CCATGTGTCAAATTAACACCCTTTATGTGTAG  328
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   298  CCATGTGTCAAATTAACGCCTTTATGTGTAG  328

```

>gb|DQ213030.1| HIV-2 isolate P2-1996 from Sweden envelope glycoprotein (env)
 gene, partial cds
 Length=1575

Sort alignments for this
 E value Score Percen
 Query start position

Score = 597 bits (323), Expect = 4e-167
 Identities = 467/533 (87%), Gaps = 24/533 (4%)
 Strand=Plus/Plus

```

Query   672  ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAA-TGGAAGGAAGCCATGCAGGAGGTGA  730
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1038  ACCCAGGCAAGCATGGTGTGGTTCAAAGGC-AAGTGGAGGGAAGCCATGCAGGAGGTAA  1096
Query   731  AGGAGACCCCTTGCGAAA-CATCCAGATATAAAGGGAA-CAGGAGCCGCACA-G-AGAAT  786
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1097  AGCAAACCCCTTGC-AAACCATACCAGATATAAA-GGAACCA--A---ATACATGAAGAAT  1149
Query   787  ATTAAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAAC  846
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1150  ATTACCTTTGAAGCACCAGGAAGAGGCTCAGACCCAGAAGTGGCATAACATGTGGACTAAT  1209

```

```

Query   847   TGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGG   906
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1210   TGCAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTAGAAAACAAA   1269

Query   907   ACGGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAA-GACAAATAATTAATACTTG   965
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1270   ACAAAATCAGATACAGCGCAATTATGTGCCATGCCATATAAAG-CAAATAATTAATACCTG   1328

Query   966   GCACAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTC   1025
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1329   GCACAAGGTAGGGAAAAATGTATATTTGCCTCCTAGGGAAGGAGAGTTGTCCTGCAATTC   1388

Query   1026   AACAGTGACCAGCATAAATTGCCAACATTGA--TAC--GGGAGATCAA-ACAGA-TATTAC   1079
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1389   CTCAGTGACCAGCATAATCGCTAACATTGACATACTAGGGA-A-CAAGAC-GAATATTAC   1445

Query   1080   CTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGA   1139
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1446   CTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTATAAATTAATAGA   1505

Query   1140   AATCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC   1192
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1506   AGTGACACCAATTGGCTTCGCACCTACATCAGAAAAGAGATACTCCTCTGCTC   1558

```

Score = 381 bits (206), Expect = 4e-102
 Identities = 288/328 (87%), Gaps = 4/328 (1%)
 Strand=Plus/Plus

```

Query   335   GCCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGA   394
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   650   GCCATTGCAACACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGA   709

Query   395   GGTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATT   454
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   710   GATTTAGATACTGTGCACCACCGGGATACATCCTACTAAGATGTAATGATACCAATTATT   769

Query   455   CAGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGA-ATGATGGAA   513
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   770   CAGGCTTTGAACCTAATTGTTCTAAAGTAGTAGCTTCTACATGCACAAGGGA-GATGGAG   828

Query   514   ACGCA-ATCTTCTACATGGTTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATAT   572
          ||||| | || | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   829   ACGCAGACCTCC-ACCTGGTTTTGGCTTTAATGGCACTAGAGCAGAAAATAGAACATATAT   887

Query   573   CTATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAC   632
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   888   CTATTGGCATGGTAGAGATAATAGGACTATTATTAGCTTAAACAAGAGTTATAGTCTCAA   947

Query   633   TATGCATTGTAAGAGGCCGGGAAATAAG   660
          || ||||| ||||| ||||| ||||| |||||
Sbjct   948   GATACATTGTAAGAGGCCAGGAAACAAG   975

```

Score = 368 bits (199), Expect = 3e-98
 Identities = 280/319 (87%), Gaps = 6/319 (1%)
 Strand=Plus/Plus

```

Query   11   GTAAGAATCAACT-GCTGATTGCTA--TTGTACTAGCTAGTGCTTACCTAACACATTGCA   67
          ||| ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   8   GTAGGAATCAACTAGTTG-TTGCCAGCTTG--CTAGCTATTGTTTGCTTAGTATATTGCA   64

Query   68   AGCAATTTGTGACTGTTTTCTATGGCATAACCGCGTGGAGGAATGCATCCATTCCCCTGT   127
          || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   65   CTCAGTATGTGACTGTTTTCTATGGCATAACCGCGTGGAGAAATGCATCCATCCCCTCT   124

Query   128   TTTGTGCAACCAAAAATAGAGATACTTGGGGAAGTGTACAGTGCTTGCCAGACAATGATG   187
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   125   TTTGTGCAACCAAAAATAGAGACACCTGGGGAACCATACAGTGCTTACCAGACAATGATG   184

Query   188   ATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCAITGGGATAATACAGTAA   247
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   185   ACTATCAGGAAATACCTTTAAATGTAACAGAGGCTTTCGACGCGTGGGATAATACAGTAA   244

Query   248   CAGAACAAGCAGTGGAGGATGCTCTGGAATCTATTTGAGACATCAATAAAACCATGTGTCA   307
          ||||| || || | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Sbjct  245  CAGAACAGGCAATAGAAGATGTCTGGAATCTATTCGAGACATCAATAAAACCATGCGTCA  304
Query   308  AATTAACACCCCTTATGTGT  326
          |||||
Sbjct  305  AATTAACACCTTTATGTGT  323

```

>gb|AF170047.1|AF170047 HIV-2 isolate 96330 from France envelope glycoprotein (e partial cds
Length=1993

Sort alignments for this
E value Score Percen
Query start position

Score = 597 bits (323), Expect = 4e-167
Identities = 464/531 (87%), Gaps = 13/531 (2%)
Strand=Plus/Plus

```

Query   669  CAA-ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAA-TGGAAGGAAGCCATGCAGGAG  726
          |||
Sbjct   585  CAAGACCCAGGCAAGCATGGTGTGGTTCAAAGGC-AAGTGGAAGGAGGCCATGCAGGAG  643

Query   727  GTGAAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAA-CAGGAGCCGCACAGAGAA  785
          |||||
Sbjct   644  GTGAAGGAAACCCTTGCAAAACATCCCAGGTATACA-GGAACCA--A-CAAAACGGAGAA  699

Query   786  TATTAAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATAACATGTGGACTAA  845
          |||||
Sbjct   700  TATTACTTTTACAGCGCCAGGAAAAGGCTCAGACCCAGAGGTGGCATAACATGTGGACTAA  759

Query   846  CTGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAG  905
          |||||
Sbjct   760  CTGCAGAGGAGAATTTTTCTACTGCAATATGACTTGGTTCCTCAATTGGGTAGAAAACAG  819

Query   906  GACGGGTCAGAAACAGCGCAATTATGCACCGTGCCATAT-AAGACAAATAATTAATACTT  964
          |||
Sbjct   820  AACGAATCAGATACGGCACAATTATGTGCCATGCCATATAAAG-CAAATAATTAATACCT  878

Query   965  GGCACAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACT  1024
          |||||
Sbjct   879  GGCACAAGGTAGGGAAAAACGTATATTTGCCTCCTAGGGAAGGAGAGTTGACCTGCACCT  938

Query  1025  CAACAGTGACCAGCATAATTGCCAACATTGA--TAC-GGGAGATCAAACAGATATTACCT  1081
          |||||
Sbjct   939  CCACAGTGACCAGCATAATTGCTAACATTGACGCACAAGAAAACCAGACAAATATTACCT  998

Query  1082  TTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAA  1141
          |||||
Sbjct   999  TTAGTGCAGAGGTGGCAGAACTATACCGATTAGAACTGGGAGATTACAAATTAATAGAGG  1058

Query  1142  TCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC  1192
          |||||
Sbjct  1059  TAACACCAATTGGCTTCGCACCTACATCAGAAAAAAGATACTCCTCTGCTC  1109

```

Score = 375 bits (203), Expect = 2e-100
Identities = 285/324 (87%), Gaps = 7/324 (2%)
Strand=Plus/Plus

```

Query   336  CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG  395
          |||||
Sbjct   202  CCATTGCAACACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG  261

Query   396  GTTTAGATACTGTGCACCACCGGGTTTGCCTACTAAGATGCAATGATATTAATTATTC  455
          |||||
Sbjct   262  GTTTAGATACTGTGCACCACCGAGCTTTGCCTACTAAGATGCAATGATACCAATTATTC  321

Query   456  AGGCTTTGCA-CCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGA-ATGATGGAA  513
          |||||
Sbjct   322  AGGCTTTG-AGCCCAACTGTTCTAAAGTAGTAGCTTCTACATGTACAAGAGAA-ATGGAA  379

Query   514  ACGCA-ATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATAT  572
          |||||
Sbjct   380  ACGCAGA-CTTCCACTTGGTTTGGCTTTAATGGCACTAGGGCGGAAAATAGAACATATAT  438

```



```

Query   573   CTATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAC   632
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   439   CTATTGGCATGGTAGAGACAATAGGACTATCATTAGCTTAAACAAGTATTATAATCTCAC   498

Query   633   TATGCATTGTAAGAGGCC-GGGAA   655
          ||| ||||| ||||| |||||
Sbjct   499   CATACGTTGTAAGAGACCAGGGAA   522

```

>gb|U05350.1|HIV2U05350 Human immunodeficiency virus type 2 isolate HIV2CBL21 gp
(env) gene, complete cds
Length=2601

Sort alignments for this
E value Score Perce
Query start position

Score = 595 bits (322), Expect = 1e-166
Identities = 463/530 (87%), Gaps = 14/530 (2%)
Strand=Plus/Plus

```

Query   670   AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAA-TGGAAGGAAGCCATGCAGGAGGT   728
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   997   AAACCCATGCAAGCATGGTGTGGTTCAAGG-TAAGTGGAGGGAAGCCATGCAGGAGGT   1055

Query   729   GAAGGAGACCCTTGCGAAACATCCCAGATATAAAGGGAA-CAGGAGCCGCACAGAGAATA   787
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1056  GAAGCAGACCCTTGTAAAACATCCCAGGTATAGA-GGAACCA--ATAAG-ACAGAAAATA   1111

Query   788   TTAAATTTAAAGCACCAGGAAGA-GGCTCAGACCCAGAAGCAGCATACATGTGGACTAAC   846
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   1112  TTACCTTTGCAGGACCAGG-AGAGGGCTCAGACCCAGAAGTGGCATAACATGTGGACTAAC   1170

Query   847   TGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGG   906
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1171  TGCAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTGGAGAACACA   1230

Query   907   ACGGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGG   966
          ||| ||||| ||| ||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Sbjct   1231  ACAAATCAGACACAACACAATTATGTGCCATGCCATATAAGGCAAATAATTAATACCTGG   1290

Query   967   CACAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCA   1026
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1291  CACAAGGTAGGGAAAAATGTATATTTGCCTCCTAGGGAAGGACTGTTGTCTCTGCAACTCA   1350

Query   1027  ACAGTGACCAGCATAATTGCCAACATTGATACG---GG-AGATCAAACAGATATTACCTT   1082
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1351  ACAGTGACCAGCATAATTGCTAACATTGATACATACGGTA-ACCAGACAGATATTACCTT   1409

Query   1083  TAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAAT   1142
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1410  TAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTATAAATTAGTAGAGAT   1469

Query   1143  CACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC   1192
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   1470  CACACCAATTGGCTTCGCACCTACATCAGTAAAAAGATACTCCTCTGCTC   1519

```

Score = 414 bits (224), Expect = 4e-112
Identities = 294/328 (89%), Gaps = 4/328 (1%)
Strand=Plus/Plus

```

Query   335   GCCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGA   394
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   608   GCCATTGCAACACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGA   667

Query   395   GGTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATT   454
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   668   GGTTTAGATACTGTGCACCACCGGGTTATGCCCTACTAAGATGCAATGATACCAATATT   727

Query   455   CAGGCTTTGCA-CCTAATTGCT-CTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGA   512
          ||||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   728   CAGGCTTTG-AGCCCAATTG-TACTAAAGTAGTAGCTTCTACATGCACAAGGATGATGGA   785

Query   513   AACGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATAT   572
          ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Sbjct  786  AACGCAAACCTCCACTTGGTTTGGCTTTAATGGCACTAGGGCAGAGAATAGAACATATAT  845
Query   573  CTATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAC  632
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  846  CTATTGGCATGGTAGGGATAATAGGACTATCATTAGCTTAAACAAGTATTATAATCTCAC  905
Query   633  TATGCATTGTAAGAGGCCGGGAAATAAG  660
        ||| ||||| ||||| ||||| |||||
Sbjct  906  TATACATTGTAAGAGGCCAGGAAACAAG  933

```

Score = 370 bits (200), Expect = 9e-99
 Identities = 284/324 (87%), Gaps = 8/324 (2%)
 Strand=Plus/Plus

```

Query   8    GTAGTAAGAATCAACTGC-TGATTGCTA--TTGTACTAGCTAGTGCTTACCTAACACATT  64
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   5    GTAGTAGGAATCTACTACTTG-TTGCCAGCTTG--CTAGCTAGTATTTGCTTAATATATT  61
Query  65    GCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGAGGAATGCATCCATTCCCC  124
        ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  62    GCACCCAGTATGTGACTGTTTTCTATGGCGTGCCCGCATGGAGAAATGCATCCATTCCCC  121
Query 125    TGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAAGTGTACAGTGCTTGCCAGACAATG  184
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 122    TCTTCTGTGCAACTAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGACAATG  181
Query 185    ATGATTATCAGGAAATAGCTTTTAAATGTAACAGAGGC-TTTCGATGCATGGGATAATACA  243
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 182    ATGATTATCAGGAAATAGCTTTGAATGTCACAGAGGCCTTT-GACGCATGGGATAATACA  240
Query 244    GTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCATGT  303
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 241    GTAACAGAACAAGCAGTGGGAAGATGTCTGGAGTCTATTTGAGACATCAATAAAACCATGC  300
Query 304    GTCAAATTAACACCCTTATGTGTA  327
        ||||| ||||| ||||| ||||| |||||
Sbjct 301    GTCAAACTGACACCTTTATGTGTA  324

```

>gb|AY509259.1| HIV-2 isolate MCN13, complete genome
 Length=9713

Sort alignments for this
 E value Score Percen
 Query start position

Score = 593 bits (321), Expect = 5e-166
 Identities = 463/528 (87%), Gaps = 23/528 (4%)
 Strand=Plus/Plus

```

Query  672  ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAA  731
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 7132  ACCCAGACAAGCATGGTGTGGTTCAAAGGTGAATGGAAGGGAGCCATGCAGGAGGTGAA  7191
Query  732  GGAGACCCTTGCGAAACATCCCAGATATAAAGGGAA-C-AGGAGCCGCACAGAGAATATT  789
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 7192  GGAAACCCTTGCAAAACATCCCAGGTATAAA-GGAACCAATGA----AACAAAGAATATT  7246
Query  790  AAATTTAAAGCACCAGG-AAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTG  848
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 7247  AACTTTACAGCACCAGGAAAG-GGCTCAGACCCAGAGGTGGCATACATGTGGACTAACTG  7305
Query  849  CAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGGAC  908
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 7306  CAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGATAG--AA-A--A-  7359
Query  909  GGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAATAATTAATACTTGGCA  968
        ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 7360  ---TAAGACACACCGCAATTATGTACCGTGCCATATAAGACAAATAATTAACACCTGGCA  7416
Query  969  CAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC  1028
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 7417  TAAGGTAGGGAAAAATGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC  7476
Query 1029  AGTGACCAGCATAATTGCCAACATTGATACG---GGAGATCAA-ACAGATATTACCTTTA  1084

```

Score = 479 bits (259), Expect = 1e-131
Identities = 303/325 (93%), Gaps = 0/325 (0%)
Strand=Plus/Plus

Score = 412 bits (223), Expect = 1e-111
Identities = 296/331 (89%), Gaps = 6/331 (1%)
Strand=Plus/Plus

```
>emb|AJ001162.1|H1J001162 Human Immunodeficiency Virus Type 2 partial envelope s
isolate sar from child in vertical transmission case
Length=1137
```

```
Sort alignments for this
E value  Score  Percen
```

Query start position

Score = 590 bits (319), Expect = 6e-165
 Identities = 477/551 (86%), Gaps = 20/551 (3%)
 Strand=Plus/Plus

Query	672	ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAA	731
Sbjct	575	ACCTAGGCAAGCATGGTGTGGTTCAAGAGGCAAATGGAAGGAAGCCATGCAGGAGGTGAA	634
Query	732	GGAGACCCCTTGCGAAACATCCCAGATATAAAGGGAAC-AGGAGCCGCA-CAGAGAATATT	789
Sbjct	635	GGAAACCCCTTGCAAAACATCCCAGGTATAAAGG-AACCACTAACA-CAAC-GA-AA-ATT	689
Query	790	AAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGC	849
Sbjct	690	AACTTTACGGCACCAGGAAAAGGCTCAGACCCAGAAGTAGAATACATGTGGACTAACTGC	749
Query	850	AGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCTCAATTGGGTAGATAACAGGAC-	908
Sbjct	750	AGAGGAGAATTTCTCTACTGCAACATGAAATGGTTCTCAATTGGATAGAAAACAAACT	809
Query	909	G-----GGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAATAATTAATACT	963
Sbjct	810	GCATCAGGTGAGAAATGGCACAATTATGTACCGTGCCATATAAGACAGATAGTTAACACC	869
Query	964	TGGCACAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAAC	1023
Sbjct	870	TGGCATAAGGTAGGGAAAAATGTATATTTGCCTCCTAGGGAAGGAGAGTTAACCTGCAAC	929
Query	1024	TCAACAGTGACCAGCATAATTGCCAACATTGATACGGG-A-GA-TCAACAGATATTACC	1080
Sbjct	930	TCAACGGTGACCAGCATAATTGCCAACATTGAGATGACTAAGAATCAAACAAATATTACC	989
Query	1081	TTTAGTGAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAA	1140
Sbjct	990	TTTAGTGAGAGGTGGCAGAACTATACCGATTAGAACTGGGGGATTATAAATTGGTAGAA	1049
Query	1141	ATCACACCAATTGGCT-TCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAG-A	1198
Sbjct	1050	ATAACACCAATTG-CTGTGCACCTACAGCAGAAAAAAGATACTCCTCTGCTCAC-AGGA	1107
Query	1199	GACATACAAGA 1209	
Sbjct	1108	GACATACAAGA 1118	

Score = 451 bits (244), Expect = 3e-123
 Identities = 299/326 (91%), Gaps = 2/326 (0%)
 Strand=Plus/Plus

Query	336	CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG	395
Sbjct	188	CCATTGCAACACATCAGTCGTCACAGAATCATGTGATGAGCACTATTGGGATGCTATGAG	247
Query	396	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATTC	455
Sbjct	248	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTGCTAAGATGCAATGATACCAATTATTC	307
Query	456	AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCT-GCTACATGCACCAGAATGATGGAAA	514
Sbjct	308	AGGCTTTGAACCAAATTGCTCTAAAGTAGTAGCTAG-TACCTGCACCAGAATGATGGAAA	366
Query	515	CGCAATCTTCTACATGGTTTTGGCTTTAATGGCACTAGAACAGAAAAATAGAACATATATCT	574
Sbjct	367	CGCAAACCTCCACGTGGTCTGGCTTTAATGGCACTAGAGCAGAAAAATAGAACATATATCT	426
Query	575	ATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTA	634
Sbjct	427	ATTGGCATGGTAGAGATAATAGAACTATAATCAGCTTAAACAAATATTATAATCTCACTT	486
Query	635	TGCATTGTAAGAGGCCGGGAAATAAG 660	
Sbjct	487	TGCATTGTAAGAGGCCAGGAAATAAG 512	

